

with A2 being clearly associated to *Braarudosphaera bigelowii*. We also found an abundant nifH sequence distantly related to *Rhizobium* but previously found in the marine environment, including off Brazil, that could constitute a new symbiotic association with oceanic phytoplankton.

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THE CROSS-KINGDOM INTERACTION IN THE MARINE MACROALGAE *ULVA*: REVISITING THE LOTTERY THEORY THROUGH CROSS-TESTING OF BACTERIA

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Green macroalgae, mainly represented by the Ulvophyceae, constitute key primary producers of estuaries and coastal marine ecosystems. *Ulva* is also an important parameter in coastal ecosystem management as it can form massive nuisance blooms (“green tides”) in shallow environments. For a deep understanding of *Ulva* species development, morphogenesis, life-cycle regulation and life-history strategies, controlled laboratory-based culture of these algae is required. *Ulva* species, like other macroalgae, harbour a rich diversity of epiphytic bacteria that promote growth and morphological development. In the absence of bacteria, algal germ cells develop into colonies consisting of undifferentiated cells with abnormal cell walls. A breakthrough in understanding how bacteria control *Ulva* development was the establishment of a standardized tripartite community consisting of *Ulva mutabilis* (Føyn) and just two isolated bacterial strains, *Roseovarius* sp. strain MS2 and *Maribacter* sp. strain MS6. Employing this standardised tripartite model system, our research aims to determine the specificity of bacteria-induced morphogenesis of *Ulva* by the cross-testing of two very well investigated *Ulva* species, the emerging model system *U. mutabilis* and the cosmopolitan and economically important species *U. intestinalis*. Specifically, the survey revealed that pairs of bacterial strains isolated from other *Ulva* sources than *U. mutabilis* and *U. intestinalis* can completely recover growth and morphogenesis of *U. mutabilis* or *U. intestinalis* gametes under axenic conditions. This study also highlights that different compositions of bacterial guilds with similar functional characteristics can enable complete algal development and thus supports the “competitive lottery” theory, implying

that assemblage of bacterial population on a specific niche (algal surface) might be random and based on presence of functional genes rather than belonging to particular taxonomic entities.

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ENVIRONMENTAL PERTURBATIONS AND CELL COMPOSITION

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Environmental perturbations are tackled by algal cells in a variety of modes that are a function of the intensity of the perturbation, its impact on metabolic processes, its duration and the growth rate.

In response to perturbation, complex acclimation response can occur. Under certain circumstances, e.g. when the reproductive advantage afforded by acclimation is limited, homeostasis can be maintained.

In this talk, I shall try to provide a panorama of the various options and describe their consequences on the physiology and the composition of microalgae.

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BIO-FOULING IN CLOSED PHOTOBIOREACTOR SYSTEMS DURING MICROALGAE CULTIVATION AS CONSEQUENCE OF ITS ASSOCIATED MICROBIOME

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Several production systems have been designed for the purpose of industrial microalgae cultivation. The ProviAPT is one of the most promising due to its novel configuration. It includes an array of vertical flat-panels enclosed

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